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#15

TECH CENTER 1600/2900

RAW SEQUENCE LISTING

DATE: 04/16/2002

PATENT APPLICATION: US/09/445,614A

TIME: 11:30:33

Input Set : A:\T1481\SL.TXT

Output Set: N:\CRF3\04162002\I445614A.raw

ENTERED

4 <110> APPLICANT: Bonnert, Timothy Peter  
 6 <120> TITLE OF INVENTION: HUMAN VANILLOID RECEPTOR-LIKE RECEPTOR  
 9 <130> FILE REFERENCE: T1481  
 11 <140> CURRENT APPLICATION NUMBER: 09/445,614A  
 12 <141> CURRENT FILING DATE: 1999-12-08  
 14 <150> PRIOR APPLICATION NUMBER: 9827016.8  
 15 <151> PRIOR FILING DATE: 1998-12-08  
 17 <160> NUMBER OF SEQ ID NOS: 19  
 19 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 2469  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Homo sapiens  
 26 <400> SEQUENCE: 1

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28	ggtcctggct	ggaccgagca	gcctcctcct	cctaggatga	cctcaccctc	cagctctcca	120
29	gttttcaggt	tggagacatt	agatggaggc	caagaagatg	gctctgaggc	ggacagagga	180
30	aagctggatt	ttgggagcgg	gctgcctccc	atggagtcac	agttccaggg	cgaggaccgg	240
31	aaattcgccc	ctcagataag	agtcaacctc	aactaccgaa	agggaaacag	tgccagtcag	300
32	ccggatccaa	accgatttga	ccgagatcgg	ctcttcaatg	cggtctcccc	gggtgtcccc	360
33	gaggatctgg	ctggacttcc	agagtacctg	agcaagacca	gcaagtacct	caccgactcg	420
34	gaatacacag	agggctccac	aggtaagacg	tgctgatga	aggctgtgct	gaaccttaag	480
35	gacggagtca	atgcctgcat	tctgccactg	ctgcagatcg	acagggactc	tggcaatcct	540
36	cagccccctg	taaatgcccc	gtgcacagat	gactattacc	gaggccacag	cgctctgcac	600
37	atcgccattg	agaagaggag	tctgcagtgt	gtgaagctcc	tggtggagaa	tggggccaat	660
38	gtgcatgccc	gggcctgcgg	ccgcttcttc	cagaagggcc	aagggaactg	cttttatctt	720
39	ggtgagctac	ccctctcttt	ggccgcttgc	accaagcagt	gggatgtggt	aagctacctc	780
40	ctggagaacc	cacaccagcc	cgccagcctg	caggccactg	actcccaggg	caacacagtc	840
41	ctgcatgccc	tagtgatgat	ctcggacaac	tcagctgaga	acattgcact	ggtgaccagc	900
42	atgtatgatg	ggctcctcca	agctggggcc	cgctctgcc	ctaccgtgca	gcttgaggac	960
43	atccgcaacc	tgcaggatct	cacgcctctg	aagctggccg	ccaaggaggg	caagatcgag	1020
44	attttcaggc	acatcctgca	gcgggagttt	tcaggactga	gccacctttc	ccgaaagtgc	1080
45	accgagtggg	gctatggggc	tgtccgggtg	tcgctgtatg	acctggcttc	tgtggacagc	1140
46	tgtgaggaga	actcagtgtc	ggagatcatt	gcctttcatt	gcaagagccc	gcaccgacac	1200
47	cgaatggtcg	ttttggagcc	cctgaacaaa	ctgctgcagg	cgaaatggga	tctgctcacc	1260
48	cccaagttct	tcttaaaact	cctgtgtaat	ctgatctaca	tgttcatctt	caccgctgtt	1320
49	gcctaccatc	agcctaccct	gaagaagcag	gccgcccctc	acctgaaagc	ggaggttgga	1380
50	aactccatgc	tgtgtacggg	ccacatcctt	atcctgctag	gggggatcta	cctcctcggt	1440
51	ggccagctgt	ggtacttctg	gcggcgccac	gtgttcatct	ggatctcggt	catagacagc	1500
52	tactttgaaa	tcctcttcct	gttccaggcc	ctgctcacag	tggtgtccca	ggtgctgtgt	1560
53	ttcctggcca	tcgagtggta	cctgcccctg	cttgtgtctg	cgctgggtgt	gggctggctg	1620
54	aacctgcttt	actatacacg	tggcttccag	cacacaggca	tctacagtgt	catgatccag	1680
55	aaggtcatcc	tgcgggacct	gctgcgcttc	cttctgatct	acttagtctt	ccttttcggc	1740

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56 ttcgctgtag ccctgggtgag cctgagccag gaggcttggc gccccgaagc tcctacaggc 1800
57 cccaatgcca cagagtcagt gcagcccatg gagggacagg aggacgaggg caacggggcc 1860
58 cagtacaggg gtatcctgga agcctccttg gagctcttca aattcaccat cggcatgggc 1920
59 gagctggcct tccaggagca gctgcacttc cgcggcatgg tgetgctgct gctgctggcc 1980
60 tacgtgctgc tcacctacat cctgctgctc aacatgctca tcgccctcat gagcgagacc 2040
61 gtcaacagtg tcgccactga cagctggagc atctggaagc tgcagaaagc catctctgtc 2100
62 ctggagatgg agaatggcta ttgggtggtg aggaagaagc agcgggcagg tgtgatgctg 2160
63 accgttggca ctaagccaga tggcagcccg gatgagcgtt ggtgcttcag ggtggaggag 2220
64 gtgaactggg ctccatggga gcagacgctg cctacgctgt gtgaggaccc gtcaggggca 2280
65 ggtgtccctc gaactctcga gaacctgtg ctggcttccc ctcccaagga ggatgaggat 2340
66 ggtgcctctg aggaaaacta tgtgcccgtc cagctcctcc agtccaactg atggcccaga 2400
67 tgcagcagga ggccagagga cagagcagag gatctttcca accacatctg ctggctctgg 2460
68 ggtccagat 2469
70 <210> SEQ ID NO: 2
71 <211> LENGTH: 824
72 <212> TYPE: PRT
73 <213> ORGANISM: Homo sapiens
75 <400> SEQUENCE: 2
76 Met Thr Ser Pro Ser Ser Ser Pro Val Phe Arg Leu Glu Thr Leu Asp
77 1 5 10 15
78 Gly Gly Gln Glu Asp Gly Ser Glu Ala Asp Arg Gly Lys Leu Asp Phe
79 20 25 30
80 Gly Ser Gly Leu Pro Pro Met Glu Ser Gln Phe Gln Gly Glu Asp Arg
81 35 40 45
82 Lys Phe Ala Pro Gln Ile Arg Val Asn Leu Asn Tyr Arg Lys Gly Thr
83 50 55 60
84 Gly Ala Ser Gln Pro Asp Pro Asn Arg Phe Asp Arg Asp Arg Leu Phe
85 65 70 75 80
86 Asn Ala Val Ser Arg Gly Val Pro Gly Ala Gly Gly Ala Thr Cys Thr
87 85 90 95
88 Gly Gly Cys Thr Gly Gly Ala Cys Thr Thr Cys Cys Ala Gly Ala Gly
89 100 105 110
90 Thr Ala Cys Cys Thr Gly Ala Gly Cys Ala Ala Gly Ala Cys Cys Ala
91 115 120 125
92 Gly Cys Ala Ala Gly Thr Ala Cys Cys Thr Cys Ala Cys Cys Gly Ala
93 130 135 140
94 Cys Thr Cys Gly Glu Asp Leu Ala Gly Leu Pro Glu Tyr Leu Ser Lys
95 145 150 155 160
96 Thr Ser Lys Tyr Leu Thr Asp Ser Glu Tyr Thr Glu Gly Ser Thr Gly
97 165 170 175
98 Lys Thr Cys Leu Met Lys Ala Val Leu Asn Leu Lys Asp Gly Val Asn
99 180 185 190
100 Ala Cys Ile Leu Pro Leu Leu Gln Ile Asp Arg Asp Ser Gly Asn Pro
101 195 200 205
102 Gln Pro Leu Val Asn Ala Gln Cys Thr Asp Asp Tyr Tyr Arg Gly His
103 210 215 220
104 Ser Ala Leu His Ile Ala Ile Glu Lys Arg Ser Leu Gln Cys Val Lys
105 225 230 235 240
106 Leu Leu Val Glu Asn Gly Ala Asn Val His Ala Arg Ala Cys Gly Arg

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107				245				250				255	
108	Phe	Phe	Gln	Lys	Gly	Gln	Gly	Thr	Cys	Phe	Tyr	Phe	Gly
109				260					265				270
110	Leu	Ser	Leu	Ala	Ala	Cys	Thr	Lys	Gln	Trp	Asp	Val	Val
111			275					280				285	
112	Leu	Glu	Asn	Pro	His	Gln	Pro	Ala	Ser	Leu	Gln	Ala	Thr
113		290					295				300		
114	Gly	Asn	Thr	Val	Leu	His	Ala	Leu	Val	Met	Ile	Ser	Asp
115	305				310					315			320
116	Glu	Asn	Ile	Ala	Leu	Val	Thr	Ser	Met	Tyr	Asp	Gly	Leu
117				325					330				335
118	Gly	Ala	Arg	Leu	Cys	Pro	Thr	Val	Gln	Leu	Glu	Asp	Ile
119			340						345				350
120	Gln	Asp	Leu	Thr	Pro	Leu	Lys	Leu	Ala	Ala	Lys	Glu	Gly
121			355					360				365	
122	Ile	Phe	Arg	His	Ile	Leu	Gln	Arg	Glu	Phe	Ser	Gly	Leu
123		370					375					380	
124	Ser	Arg	Lys	Phe	Thr	Glu	Trp	Cys	Tyr	Gly	Pro	Val	Arg
125	385				390					395			400
126	Tyr	Asp	Leu	Ala	Ser	Val	Asp	Ser	Cys	Glu	Glu	Asn	Ser
127				405					410				415
128	Ile	Ile	Ala	Phe	His	Cys	Lys	Ser	Pro	His	Arg	His	Arg
129			420						425				430
130	Leu	Glu	Pro	Leu	Asn	Lys	Leu	Leu	Gln	Ala	Lys	Trp	Asp
131			435					440				445	
132	Pro	Lys	Phe	Phe	Leu	Asn	Phe	Leu	Cys	Asn	Leu	Ile	Tyr
133		450					455				460		
134	Phe	Thr	Ala	Val	Ala	Tyr	His	Gln	Pro	Thr	Leu	Lys	Lys
135	465				470					475			480
136	Pro	His	Leu	Lys	Ala	Glu	Val	Gly	Asn	Ser	Met	Leu	Leu
137				485					490				495
138	Ile	Leu	Ile	Leu	Leu	Gly	Gly	Ile	Tyr	Leu	Leu	Val	Gly
139			500						505				510
140	Tyr	Phe	Trp	Arg	Arg	His	Val	Phe	Ile	Trp	Ile	Ser	Phe
141			515						520				525
142	Tyr	Phe	Glu	Ile	Leu	Phe	Leu	Phe	Gln	Ala	Leu	Leu	Thr
143		530					535					540	
144	Gln	Val	Leu	Cys	Phe	Leu	Ala	Ile	Glu	Trp	Tyr	Leu	Pro
145	545				550					555			560
146	Ser	Ala	Leu	Val	Leu	Gly	Trp	Leu	Asn	Leu	Leu	Tyr	Tyr
147				565					570				575
148	Phe	Gln	His	Thr	Gly	Ile	Tyr	Ser	Val	Met	Ile	Gln	Lys
149			580						585				590
150	Arg	Asp	Leu	Leu	Arg	Phe	Leu	Leu	Ile	Tyr	Leu	Val	Phe
151			595					600				605	
152	Phe	Ala	Val	Ala	Leu	Val	Ser	Leu	Ser	Gln	Glu	Ala	Trp
153		610					615				620		
154	Ala	Pro	Thr	Gly	Pro	Asn	Ala	Thr	Glu	Ser	Val	Gln	Pro
155	625				630					635			640

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156 Gln Glu Asp Glu Gly Asn Gly Ala Gln Tyr Arg Gly Ile Leu Glu Ala
157                               645                               650                               655
158 Ser Leu Glu Leu Phe Lys Phe Thr Ile Gly Met Gly Glu Leu Ala Phe
159                               660                               665                               670
160 Gln Glu Gln Leu His Phe Arg Gly Met Val Leu Leu Leu Leu Ala
161                               675                               680                               685
162 Tyr Val Leu Leu Thr Tyr Ile Leu Leu Leu Asn Met Leu Ile Ala Leu
163                               690                               695                               700
164 Met Ser Glu Thr Val Asn Ser Val Ala Thr Asp Ser Trp Ser Ile Trp
165 705                               710                               715                               720
166 Lys Leu Gln Lys Ala Ile Ser Val Leu Glu Met Glu Asn Gly Tyr Trp
167                               725                               730                               735
168 Trp Cys Arg Lys Lys Gln Arg Ala Gly Val Met Leu Thr Val Gly Thr
169                               740                               745                               750
170 Lys Pro Asp Gly Ser Pro Asp Glu Arg Trp Cys Phe Arg Val Glu Glu
171                               755                               760                               765
172 Val Asn Trp Ala Ser Trp Glu Gln Thr Leu Pro Thr Leu Cys Glu Asp
173                               770                               775                               780
174 Pro Ser Gly Ala Gly Val Pro Arg Thr Leu Glu Asn Pro Val Leu Ala
175 785                               790                               795                               800
176 Ser Pro Pro Lys Glu Asp Glu Asp Gly Ala Ser Glu Glu Asn Tyr Val
177                               805                               810                               815
178 Pro Val Gln Leu Leu Gln Ser Asn
179                               820
181 <210> SEQ ID NO: 3
182 <211> LENGTH: 51
183 <212> TYPE: DNA
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: Primer
189 <400> SEQUENCE: 3
190 tgttaccaat ctgaagtggg agcggccgcc tcattttttt tttttttttt t
192 <210> SEQ ID NO: 4
193 <211> LENGTH: 21
194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <223> OTHER INFORMATION: PCR Primer
200 <400> SEQUENCE: 4
201 caggcccggg catgcacatt g
203 <210> SEQ ID NO: 5
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205 <212> TYPE: DNA
206 <213> ORGANISM: Artificial Sequence
208 <220> FEATURE:
209 <223> OTHER INFORMATION: PCR Primer
211 <400> SEQUENCE: 5
212 ccagggcgag gaccggaaat t
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51

21

21

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DATE: 04/16/2002

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Input Set : A:\Tl481 SL.TXT

Output Set: N:\CRF3\04162002\I445614A.raw

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215 <211> LENGTH: 21
216 <212> TYPE: DNA
217 <213> ORGANISM: Artificial Sequence
219 <220> FEATURE:
220 <223> OTHER INFORMATION: PCR Primer
222 <400> SEQUENCE: 6
223 gacagctgga gcatctggaa g 21
225 <210> SEQ ID NO: 7
226 <211> LENGTH: 21
227 <212> TYPE: DNA
228 <213> ORGANISM: Artificial Sequence
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231 <223> OTHER INFORMATION: PCR Primer
233 <400> SEQUENCE: 7
234 gacagctgga gcatctggaa g 21
236 <210> SEQ ID NO: 8
237 <211> LENGTH: 21
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial Sequence
241 <220> FEATURE:
242 <223> OTHER INFORMATION: PCR Primer
244 <400> SEQUENCE: 8
245 cttccagatg ctccagctgt c 21
247 <210> SEQ ID NO: 9
248 <211> LENGTH: 21
249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
253 <223> OTHER INFORMATION: PCR Primer
255 <400> SEQUENCE: 9
256 tttgccacca gaattcactg g 21
258 <210> SEQ ID NO: 10
259 <211> LENGTH: 21
260 <212> TYPE: DNA
261 <213> ORGANISM: Artificial Sequence
263 <220> FEATURE:
264 <223> OTHER INFORMATION: PCR Primer
266 <400> SEQUENCE: 10
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269 <210> SEQ ID NO: 11
270 <211> LENGTH: 21
271 <212> TYPE: DNA
272 <213> ORGANISM: Artificial Sequence
274 <220> FEATURE:
275 <223> OTHER INFORMATION: PCR Primer
277 <400> SEQUENCE: 11
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280 <210> SEQ ID NO: 12
281 <211> LENGTH: 21

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VERIFICATION SUMMARY

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